Zika preventive measures. Using mosquito repellent was mentioned most frequently, more so than other available options, such as postponing travel to areas with local Zika activity or wearing long-sleeved shirts or pants. This finding makes sense because half of all preventive measure posts originate with commercial accounts, which often are promoting mosquito repellents. In addition, using mosquito repellent is not a complex behavior, and few barriers to its use likely exist beyond mild inconvenience. However, when a Zika vaccine becomes available, the conversation about Zika preventive measures on Instagram will likely change because vaccination is not without controversy. Finally, cues to action were present in only 10.2% of the sample, and cues to self-efficacy were present in only 9.6% of the sample. Public health communications professionals should focus on increasing these forms of messaging on social media, especially when a vaccine becomes available.

Overall, the Zika-focused posts in this sample reflected a high level of perceived threat and a low level of expressed self-efficacy. At least some of the responses seem to be maladaptive in nature. To counter this trend, public health organizations should consider increasing their activity regarding Zika prevention on Instagram. For example, they could emphasize the benefits and relative ease of restricting travel to high-risk areas, using repellent, and wearing protective clothing—and that the benefits of such actions outweigh the barriers. Because the salience of Zika tends to wane after the summer, cues to action are particularly needed to remind the public of ongoing risk, especially travel-related risk. Last, once a vaccine becomes available, it will be essential to promote the safety and efficacy of the vaccine and counter misinformation about vaccination side effects more generally.

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Zoonotic Endocarditis in a Man, the Netherlands

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In 2017, endocarditis caused by *Streptococcus equi* subspecies *zooepidemicus* was diagnosed in a man in the Netherlands who had daily contact with horses. Whole-genome sequencing of isolates from the man and his horses confirmed the same clone, indicating horse-to-human transmission. Systematic reporting of all zoonotic cases would help with risk assessment.

On July 23, 2017, a 62-year-old man sought care at the emergency department of Tergooi Hospital (Hilversum, the Netherlands) for general malaise and fever up to

40.6°C (105.1°F). Nine months earlier, the patient's aortic valve had been replaced with a mechanical prosthesis. The emergency department staff found no cause for his complaints. Blood test results suggested an active infection; C-reactive protein concentration was 250 mg/L (reference value <10 mg/L). Blood culture grew gram-positive cocci, which were identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (Microflex LT; Bruker, http://www.bruker.com) as S*treptococcus equi* subspecies *zooepidemicus.* The MIC for penicillin was 0.016 and for gentamicin was 16 mg/L.

Cardiac ultrasonography revealed a small, mobile structure adhering to the aortic valve prosthesis, at the side of the left ventricle outflow tract, which was possibly bacterial vegetation. An abscess was present in the aortic root at the side of the left coronary artery. The diagnosis was bacterial endocarditis of the prosthetic valve caused by *S. equi* subsp. *zooepidemicus.*

The patient received high doses of penicillin (2 million IU/4 h for 6 wk) and gentamicin (3 mg/kg/24 h for 2 wk) intravenously, according to national guidelines (https://www.swab.nl/richtlijnen). Results of subsequent blood cultures taken on days 4 and 8 after admission were negative, and the patient was discharged after 6 weeks of treatment.

Several case reports have described the potential for *S. equi* subsp. *zooepidemicus* to cause severe infection in humans. Contact with horses is a possible source of infection (*1*–*5*). The patient we describe had frequent contact with 7 horses stabled in his yard. Two weeks before his hospital admission, horse A showed signs of an upper airway infection: copious bilateral purulent nasal discharge, coughing, and fever up to 39.1°C (102.4°F; reference range 37.5°C–38.3°C [99.5°F–100.9°F]). Seventeen days later, horse B showed similar signs. After a nasal swab sample from horse B tested by the Animal Health Service (Deventer, the Netherlands) had a negative PCR result for *S. equi* subsp. *equi*, we collected nasal swab samples from all 7 horses and cultured them for streptococci on blood agar (Oxoid, http://www.oxoid.com) at 37°C for 48 h. Culture results were positive for *S. equi* subsp. *zooepidemicus* for 4 of the 7 horses. Horses A and B recovered uneventfully without antimicrobial drug treatment.

To investigate the relatedness of isolates, we fully sequenced 2 isolates from horse A, 4 isolates from horse B, 2 isolates from horse C, 1 isolate from horse D, and 1 isolate from the human patient. We identified sequence type (ST) 212 in 1 isolate from horse A, all 4 isolates from horse B, the 2 isolates from horse C, and the isolate from the patient (Appendix Table, https://wwwnc.cdc.gov/EID/article/25/1/18-1029-App1.pdf). All genomes were aligned with a selection of publicly available *S. equi* subsp. *zooepidemicus* isolates. We constructed a core-genome alignment of 1.55 Mb, representing 76% of the genome of the reference isolate MGCS10565. Comparison of the *S. equi* subsp. *zooepidemicus* core genomes showed that the human and animal ST212 isolates had 100% identical core genomes (Appendix Figure), strongly suggesting that the same clone was present in the human patient and the animals. Construction of core-genome alignments of the ST212 isolates resulted in a 1.94-Mb core genome, 97% of the genome of the ST212 isolates; only 3% of the genome was located in the accessory genome. We extracted single-nucleotide polymorphisms (SNPs) that differed between these isolates and used them to generate a minimal-spanning tree (Figure). The number of SNPs between the human and horse isolates did not differ significantly from the number of SNPs differing between horse isolates, thereby demonstrating animal-to-human transmission of *S. equi* subsp. *zooepidemicus*.

In healthy horses, *S. equi* subsp. *zooepidemicus* is a commensal organism of the upper respiratory and lower genital tracts and can cause secondary infections (*6*). However, in 2010, a large outbreak in Iceland showed that *S. equi* subsp. *zooepidemicus* might be a primary pathogen that spreads clinically among horses without any other predisposing factors (*7*). Infections with *S. equi* subsp. *zooepidemicus* in humans, especially confirmed cases originating from contact with horses, are rare. Only a few reports confirm a horse as the source of infection by whole-genome sequencing (*7*,*8*). Systematic reporting of suspected or confirmed transmission of pathogens between horses and humans is lacking. Such reporting would support the estimation of the burden of equine-origin zoonotic infections in humans, which is needed as the equine industry continues to grow. Collaboration among disciplines to develop such a reporting system is fundamental for enabling reliable assessment of the potential risk for humans to become ill after contact with horses and the usefulness of implementing precautionary measures for patients with specific conditions.

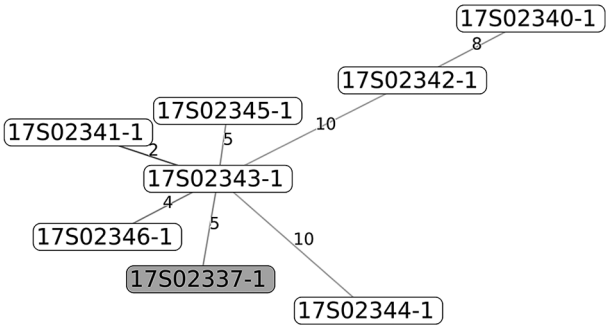

Figure. Minimal-spanning tree of 34 single-nucleotide polymorphisms. Gray indicates the human isolate. Single-nucleotide polymorphisms counts are given.

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Trachoma in 3 Amerindian Communities, Venezuelan Amazon, 2018

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Trachoma is among the most common infectious causes of blindness. During January–May 2018, a total of 4 trachoma cases were diagnosed among Amerindians of the Yanomami ethnic group in 3 communities of southern Venezuela. This country has social and environmental conditions conducive to the endemicity of this neglected tropical disease.

Trachoma, caused by the bacterium *Chlamydia trachomatis*, is the most common infectious cause of blindness. It is endemic to many of the poorest and most remote areas of Africa, Asia, Australia, the Middle East, and Latin America (*1*). Trachoma causes visual impairment in ≈2.2 million persons worldwide, of whom 1.2 million are completely blind (*2*). As of April 2018, ≈158 million persons living in districts to which trachoma is endemic are at risk (*3*). In South America, trachoma is considered endemic to Brazil (*4*) and Colombia (*5*) but not to Venezuela. We describe 4 patients in whom trachoma was diagnosed during January–May 2018 in 3 communities in the Amazon region of southern Venezuela. All were Amerindians of the Yanomami ethnic group living near rivers in extensive, well-conserved international forest frontiers.

During January–May 2018, in the integrated healthcare system in the Venezuela states of Amazonas and Bolivar, 4 trachoma cases were detected. Two cases occurred in the Yanomami community of Kuyuwiniña, Alto Caura River basin, Bolivar, and 1 case occurred in each of 2 communities of the upper Orinoco River basin of Amazonas (Oroshi and Rashakami) (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/25/1/18-1362-App1.pdf).

Case-patient 1 was a 38-year-old woman from Oroshi with a 5-month history of trachomatous trichiasis (TT), pain, madarosis, blepharitis, and conjunctivitis in both eyes. Case-patient 2 was a 35-year-old woman from Kuyuwiniña with a 6-month history of TT, pain, madarosis, blepharitis, and conjunctivitis in both eyes; corneal opacity in the right eye; and full blindness in the left eye (Appendix Figure 2). Case-patient 3 was a 45-year-old man from Kuyuwiniña with a 5-year

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Appendix

Supplementary Methods

DNA was isolated using the MO-BIO Ultra Clean Microbial DNA isolation kit (MO-BIO Laboratories INC, Carlsbad, CA). Sequencing was performed using Illumina NextSeq with 150 bp paired end reads, that were assembled using SPAdes 3.10.1 (*1*). The average coverage was 90x. The quality of genomes obtained in this study and the downloaded genomes was assessed with CheckM (*2*). Only genomes with >98% completeness score were included. The whole genome sequence data of the isolates have been deposited at the Short Read Archive under project PRJEB27317 with the accession numbers listed in the Appendix Table. A core-genome alignment using Parsnp v1.2 (*3*) on contigs larger than 2 kbp was performed to construct phylogenetic maximum likelihood trees using FastTree2 (*4*) and visualized with FigTree (http://tree.bio.ed.ac.uk/software/figtree/). Genomes were annotated with Prokka (*5*) and orthology was determined using Roary (*6*).

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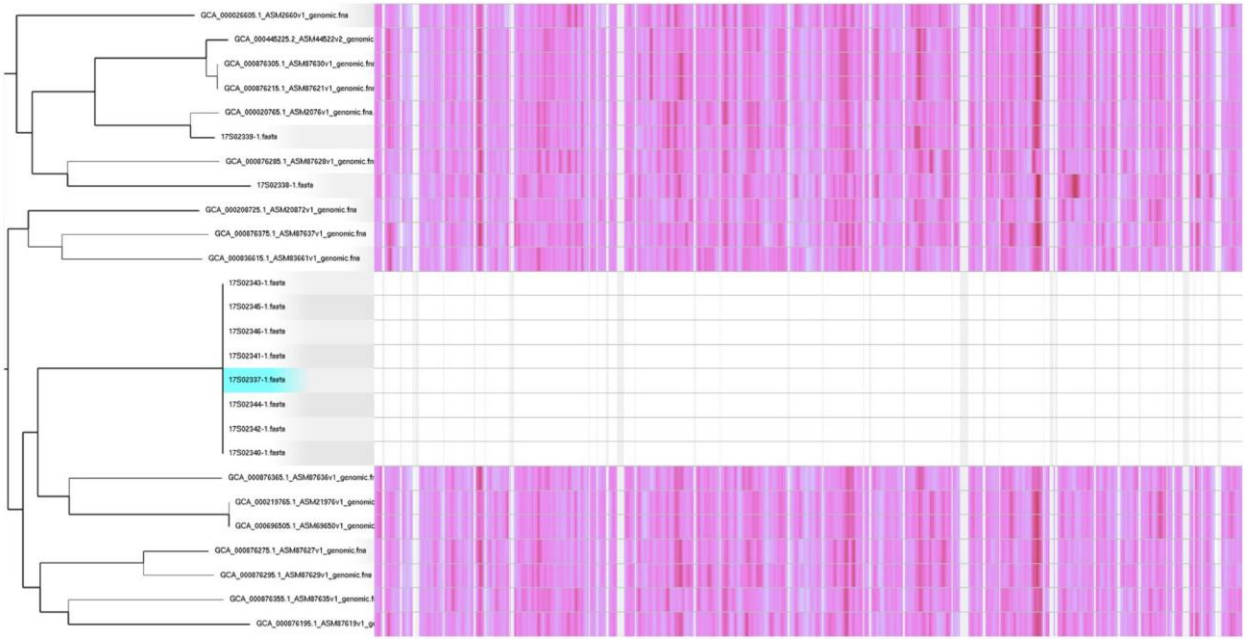
Appendix Table. *Strep. Equi.* subsp. *Zooepidemicus* strains investigated by whole genome sequencing

Strain	Source	MLST type	Coverage	Accession	Reference	Assembly
17S02337–1	human	212	85	ERS2550930		
17S02338–1	horse D	92	83	ERS2550931		
17S02339–1	horse A	99	100	ERS2550932		
17S02340–1	horse A	212	95	ERS2550933		
17S02341–1	horse B	212	99	ERS2550934		
17S02342–1	horse B	212	92	ERS2550935		
17S02343–1	horse B	212	85	ERS2550936		
17S02344–1	horse B	212	68	ERS2550937		
17S02345–1	horse C	212	69	ERS2550938		
17S02346–1	horse C	212	95	ERS2550939		
MGCS10565		72		CP001129.1	ref	GCA_000020765.1_ASM2076v1
H70		1		FM204884.1	ref	GCA_000026605.1_ASM2660v1
BHS5		123		CABY01000011.1	ref	GCA_000208725.1_ASM20872v1
ATCC35246		194		CP002904.1	ref	GCA_000219765.1_ASM21976v1
SzS31A1		279		AUXA02000089.1	ref	GCA_000445225.2_ASM44522v2
CY		194		CP006770.1	ref	GCA_000696505.1_ASM69650v1
2329		-		JTJH01000001.1	ref	GCA_000836615.1_ASM83661v1
Sz105		140		JATZ01000041.1	ref	GCA_000876195.1_ASM87619v1
Sz4is		279		JAUE01000033.1	ref	GCA_000876215.1_ASM87621v1
SzAM35		65		JATY01000119.1	ref	GCA_000876275.1_ASM87627v1
SzAM60		-		JATX01000052.1	ref	GCA_000876285.1_ASM87628v1
Sz16		156		JATW01000074.1	ref	GCA_000876295.1_ASM87629v1
Sz12is		279		JAUD01000037.1	ref	GCA_000876305.1_ASM87630v1
Sz5		303		JAUC01000036.1	ref	GCA_000876355.1_ASM87635v1
Sz35		203		JAUB01000112.1	ref	GCA_000876365.1_ASM87636v1
Sz57		96		JAUA01000048.1	ref	GCA_000876375.1_ASM87637v1



Appendix Figure. Phylogenetic tree and single-nucleotide polymorphism locations of whole-genome alignment data of human, horse, and reference isolates. Blue shading, human isolate; purple, single-nucleotide polymorphisms; gray, DNA regions that were excluded from the analysis.